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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:18:03 ; Search time 1484.97 Seconds
(without alignments)
12007.805 Million cell updates/sec

Title: US-09-807-933B-4

Perfect score: 1101
Sequence: 1 atgaagttacttactattac.....caggtgttcaagaataa 1101

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estcin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hrc:*
9: gb_estl:*
10: gb_estc2:*
11: gb_hrc:*
12: gb_estc3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	164.6	15.0	691	10	BE585661
2	127.6	11.6	450	13	BE585661
3	119	10.8	444	13	BE585661
4	113.2	10.3	426	13	BE585661
5	75	6.8	215	13	BE585661
6	58.2	5.3	289	13	BE585661

Result No.	Score	Query Match	Query length	DB ID	Description
7	58.2	5.3	299	13	BE585661
8	57	5.2	274	13	BE585661
9	57	5.2	280	13	BE585661
10	57	5.2	289	13	BE585661
11	49.2	4.5	559	9	BE585661
12	46.8	4.3	541	14	BE585661
13	45.6	4.1	243	10	BE585661
14	44	4.0	539	9	BE585661
15	44	4.0	558	10	BE585661
16	43.8	4.0	406	10	BE585661
17	43.8	4.0	500	10	BE585661
18	43	3.9	806	17	BE585661
19	42.8	3.9	989	17	BE585661
20	42.2	3.8	805	17	BE585661
21	41.6	3.8	381	10	BE585661
22	41.2	3.7	478	13	BE585661
23	41.2	3.7	490	13	BE585661
24	41.2	3.7	684	14	BE585661
25	41.2	3.7	714	9	BE585661
26	41.2	3.7	716	13	BE585661
27	41.2	3.7	748	17	BE585661
28	40.8	3.7	450	17	BE585661
29	40.6	3.7	547	17	BE585661
30	40.6	3.7	605	10	BE585661
31	40.6	3.7	619	17	BE585661
32	40.4	3.7	280	13	BE585661
33	40.4	3.7	481	13	BE585661
34	40.4	3.7	773	17	BE585661
35	40.4	3.7	824	17	BE585661
36	40.2	3.7	470	13	BE585661
37	40.2	3.7	540	13	BE585661
38	40	3.6	550	17	BE585661
39	39.8	3.6	451	17	BE585661
40	39.8	3.6	476	13	BE585661
41	39.8	3.6	482	13	BE585661
42	39.8	3.6	491	13	BE585661
43	39.8	3.6	933	17	BE585661
44	39.8	3.6	979	17	BE585661
45	39.6	3.6	459	13	BE585661

ALIGNMENTS

RESULT 1
LOCUS BE585661
DEFINITION EST#6PSP6_D02_d2_014 KSU wheat Fusarium graminearum infected spike
CDNA library Triticum aestivum cDNA clone EST#6PSP6_D02_d2_014,
mRNA sequence.
ACCESSION BE585661
VERSION BE585661.1 GI:9838604
KEYWORDS
SOURCE
ORGANISM
broad wheat.
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticaceae; Triticum.
REFERENCE
Fellers, J.P., Li, W.L., Hill-Ambroz, K., Matthews, A., and Gill, B.S.
The structure and function of the expressed portion of the wheat
genomes - Kansas State University. Fusarium graminearum infected
spike cDNA library
Unpublished (2000)
Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
Email: jpf@alfalfa.ksu.edu
Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20
Seq primer: SP6.
Location/Qualifiers

FEATURES
source
1..691
/organism="Triticum aestivum"
/cultivar="Suma13"
/db_xref="taxon:4565"
/clone="ESTH6BSP6.D02.d2.014"
/clone_lib="KSU wheat Fusarium graminearum infected spike
cDNA library"

/tissue_type="Spike"
/dev_stage="Adult Plant"
/lab_host="E. coli JM109"
/note="Vector: pGEM-T easy; Site 1: SacII; Site 2: SpeI;
plants were grown in the greenhouse. Spikes were sprayed
with Fusarium graminearum (at what stage). Total RNA, and
poly(A) RNA were prepared from infected spikes. cDNA was
prepared using the SmartTM PCR cDNA synthesis kit from
Clontech. cDNA was cloned into the pGEM-T easy vector
from Promega."

BASE COUNT 135 a 196 c 163 g 197 t
ORIGIN

Query Match 15.0%; Score 164.6; DB 10; Length 691;
Best Local Similarity 62.0%; Pred. No. 1.3e-37;
Matches 282; Conservative 0; Mismatches 164; Indels 9; Gaps 1;

464 GTGGGCGCTGTGTAAGCGTGTCACTACTGCTATTGGAATGCTGTAAAGGCTCTCTGTA 523
160 GTGCTGCTTGTGGAAGTGTCACTCTGATCTGGACTGTCGACGCTTCTTGTCT 219
524 GCTGCGCCGGTAAGCCCAATGTCAGTTCTCTGTCAAGTCTGTAAAGATGTGTCA 583
220 CTTGAGAGGCGCAAGCCCAAGTCCAGCCCTCTGCTTGAAGTGTGACAAAAGACAAAC 279
584 CTGCGCTTGTGTAAGCGTGTCACTACTGCTATTGGAATGCTGTAAAGGCTCTCTGTA 643
280 CCATCACTTAACTGAAAGCGCTTCAAGGTTGTGAGAGTGTGTGCTTGTCTTGTGA 339
644 ACACAAACGAGCTTGGGCTGTAAAGATCTTGCCTATGTTGGCTGCTGCTGCA 703
340 CTACACTACCTCCCTTGGGCTGTCAAGCAAGACCTTGTAGGTTTCACTGCTCAAGC 399
704 TCAGTGTGTGTGTAATCTGCTGTGCTTCTTGTGAACTTCACTTCACTTCA 763
400 TTGCTGTGTGCACTGACCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 459
764 CCTGTGTGTGTGTAAGATGTGTATTCAGATCACTTACCTGTGTGTGTGTGTGTGT 823
460 GTCCCGTAAGGGAAGATGATGTGTCCAGTCCACCAACTGTGTGTGTGTGTGTGTGT 517
824 CTTCTACTGTGTCTTGAATGCAATGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 883
518 -----TGATTAACCACTTGAATGATGCGCGGTGTGTGTGTGTGTGTGTGTGTGT 570
884 GTTGTCTCAAGCAATGGGTGTCTCCCAATGACGCT 918
Db 571 GATGCACTCTGATGTTCGCAAGCCCTCGTGTGT 605

RESULT 2
BI200729 450 bp mRNA linear EST 10-JUL-2001
LOCUS
DEFINITION
B1200729.1 GI:14666701
Fusarium sporotrichioides T1 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone 01f05f5 5', mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
B1200729.1 GI:14666701
EST.
Fusarium sporotrichioides.
Fusarium sporotrichioides
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 450)
Ren, Q., Tag, A., Peplov, A., Lai, H., Kupfer, C., Peterson, A., Beremand
, M. and Roe, B. Fusarium sporotrichioides EST database
Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability. Included
is the best homolog from a blast search of Genbank nr 04-09-01
633 5e-66 g11170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
KPRECURSOR (EN
KPRECURSOR (EN
Seq primer: T3
High quality sequence stop: 440.

FEATURES
source
1..450
/organism="Fusarium sporotrichioides"
/strain="T1 10"
/db_xref="taxon:5514"
/clone_lib="Fusarium sporotrichioides T1 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 90 a 125 c 102 g 133 t
ORIGIN

Query Match 11.6%; Score 127.6; DB 13; Length 450;
Best Local Similarity 62.0%; Pred. No. 1e-26;
Matches 202; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

464 GTGGGCGCTGTGTAAGCGTGTCACTACTGCTATTGGAATGCTGTAAAGGCTCTCTGTA 523
124 GTGCTGCTTGTGGAAGTGTCACTCTGATCTGGACTGTCGACGCTTCTTGTCT 183
524 GCTGCGCCGGTAAGCCCAATGTCAGTTCTCTGTCAAGTCTGTAAAGATGTGTCA 583
184 CTTGAGAGGCGCAAGCCCAAGTCCAGCCCTCTGCTGTGATGTGACAAAAGATTAAC 243
584 CTGCGCTTGTGTAAGCGTGTCACTACTGCTATTGGAATGCTGTAAAGGCTCTCTGTA 643
244 CTATCACTTAACTGAAAGCGCTTCAAGGTTGTGAGAGTGTGTGCTTGTGTGTGA 303
644 ACACAAACGAGCTTGGGCTGTAAAGATCTTGCCTATGTTGGCTGCTGCTGCA 703
304 CCATCACTACCTCCCTTGGGCTGTCAAGCAAGACCTTGTAGGTTTGGCTTACCAAGC 363
704 TCAGTGTGTGTGTAATCTGCTGTGCTTCTTGTGAACTTCACTTCACTTCA 763
364 TTGCTGTGTGTGTAAGCGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 423
764 CCTGTGTGTGTGTAAGATGTGT 789
Db 424 GTCCCGTAAGGGAAGATGATTT 449

RESULT 3
BI190695 444 bp mRNA linear EST 10-JUL-2001
LOCUS
DEFINITION
B1190695.1 GI:14664374
Fusarium sporotrichioides T1 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone 13f0f5 5', mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
B1190695.1 GI:14664374
EST.
Fusarium sporotrichioides.
Fusarium sporotrichioides
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

REFERENCE 1 (bases 1 to 444)
 AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
 TITLE Analysis of a Fusarium sporotrichioides EST database
 JOURNAL Unpublished (2001)
 COMMENT Contact: Bruce A. Roe, University of Oklahoma, broeou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broeou.edu
 Contact Dr. Marian Beremand regarding clone availability. Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 576 3e-59 g|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
 KRECURSOR EN
 Seq primer: T3.
 Location/Qualifiers
 1..444
 /organism="Fusarium sporotrichioides"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="139101s"
 /clone_1id="Fusarium sporotrichioides Tri 10 overexpressed
 cdna library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; 5' end of CDNA cloned into EcoRI site of pBluescript
 ; 3' end of CDNA cloned into XhoI site of pBluescript"

BASE COUNT 85 a 127 c 92 g 140 t
 ORIGIN

Query Match 10.8%; Score 119; DB 13; Length 444;
 Best Local Similarity 62.7%; Pred. No. 3.7e-24;
 Matches 185; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

Qy 464 GTGTGCTCTGTGTAACGGTGTCTACTCTGTAATGGAGTGTGAAGCCTTCCTGA 523
 Db 150 GTGTGCTCTGTGTAAGTGGCACTCTACTGATGTGGAAGTGTGCAAGCTTCTGCT 209
 Qy 524 GCTGGCCGGTAAGGCCAATGTCACTTCTCTGAATCCTGTAAACAAGATGTGTCA 583
 Db 210 CTGGAGGGGCAAGGCTAAAGTCAAGCGCCCTGCTGACTGTGCAACAAGATAACC 269
 Qy 584 CTGGCTTAGTGACAGCAATGTCGAAGTGTGAAGGTGTGAACAGTAACTGTGA 643
 Db 270 CTATCTACTAACCTGAACGCTGTCAACGCTGTGAAGGTGTGTCTCTATATGCTTCA 329
 Qy 644 ACGACAACACGCTTGGCTGTAAAGATAATCTTGCCTATAGTTCGCTGCTGCCA 703
 Db 330 CCAACTACTCCCGGCGCTGTCAACAGACCTTGTTCGCTTCCCTGTACCAAGC 389
 Qy 704 TCACTGTGTGTGTGAATCTCGCTGTGCTGTCTTCTTGTTCGAATTAATTCTTAC 758
 Db 390 TTGCTGTGTGTGTGAAGCCAGCTGTGCTGTCTGTCTATGCTCTACCTTCAAC 444

RESULT 4
 B1187295 426 bp mRNA linear EST 10-JUL-2001
 LOCUS alh1lf.r1 Fusarium sporotrichioides Tri 10 overexpressed CDNA
 DEFINITION library Fusarium sporotrichioides CDNA clone alh1lf 5', mRNA
 sequence.
 ACCESSION B1187295 GI:14660974
 VERSION B1187295.1
 KEYWORDS EST.
 SOURCE Fusarium sporotrichioides.
 ORGANISM Fusarium sporotrichioides.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium.
 REFERENCE 1 (bases 1 to 426)
 AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
 TITLE Analysis of a Fusarium sporotrichioides EST database
 JOURNAL Unpublished (2001)

TITLE Analysis of a Fusarium sporotrichioides EST database
 JOURNAL Unpublished (2001)
 COMMENT Other ESTs: alh1lf.f1
 Contact: Bruce A. Roe, University of Oklahoma, broeou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broeou.edu
 Contact Dr. Marian Beremand regarding clone availability. Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 565 5e-58 g|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
 KRECURSOR EN
 Seq primer: T3.
 High quality sequence stop: 338.
 Location/Qualifiers
 1..426
 /organism="Fusarium sporotrichioides"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="alh1lf"
 /clone_1id="Fusarium sporotrichioides Tri 10 overexpressed
 cdna library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; 5' end of CDNA cloned into EcoRI site of pBluescript
 ; 3' end of CDNA cloned into XhoI site of pBluescript"

BASE COUNT 82 a 119 c 91 g 134 t
 ORIGIN

Query Match 10.3%; Score 113.2; DB 13; Length 426;
 Best Local Similarity 62.2%; Pred. No. 1.9e-22;
 Matches 178; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

Qy 464 GTGTGCTCTGTGTAACGGTGTCTACTCTGTAATGGAGTGTGAAGCCTTCCTGA 523
 Db 140 GTGTGCTCTGTGTAAGTGGCACTCTACTGATGTGGAAGTGTGCAAGCTTCTGCT 199
 Qy 524 GCTGGCCGGTAAGGCCAATGTCACTTCTCTGAATCCTGTAAACAAGATGTGTCA 583
 Db 200 CTGGAGGGGCAAGGCTAAAGTCAAGCGCCCTGCTGACTGTGCAACAAGATAACC 259
 Qy 584 CTGGCTTAGTGACAGCAATGTCGAAGTGTGAAGGTGTGAACAGTAACTGTGA 643
 Db 260 CTATCTACTAACCTGAACGCTGTCAACGCTGTGAAGGTGTGTCTCTATATGCTTCA 319
 Qy 644 ACGACAACACGCTTGGCTGTAAAGATAATCTTGCCTATAGTTCGCTGCTGCCA 703
 Db 320 CCAACTACTCCCGGCGCTGTCAACAGACCTTGTTCGCTTCCCTGTACCAAGC 379
 Qy 704 TCACTGTGTGTGTGAATCTCGCTGTGCTGTCTTCTTGTTCGAATTAATTCTTAC 749
 Db 380 TTGCTGTGTGTGTGAAGCCAGCTGTGCTGTCTGTCTATGCTCT 425

RESULT 5
 B1190568 215 bp mRNA linear EST 10-JUL-2001
 LOCUS 12el1f.r1 Fusarium sporotrichioides Tri 10 overexpressed CDNA
 DEFINITION library Fusarium sporotrichioides CDNA clone 12el1f 5', mRNA
 sequence.
 ACCESSION B1190568 GI:14664247
 VERSION B1190568.1
 KEYWORDS EST.
 SOURCE Fusarium sporotrichioides.
 ORGANISM Fusarium sporotrichioides.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium.
 REFERENCE 1 (bases 1 to 215)
 AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
 TITLE Analysis of a Fusarium sporotrichioides EST database
 JOURNAL Unpublished (2001)

COMMENT

Other ESTs: j2ellfs.f1
 Contact: Bruce A. Roe, University of Oklahoma, broeou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broeou.edu
 Contact Dr. Marian Beremand regarding clone availability. Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 363 7e-35 g1|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
 KPRECURSOR (EN
 KPRECURSOR (EN
 Seq primer: T3
 High quality sequence stop: 156.
 Location/Qualifiers

FEATURES

source

1. .215
 /organism="Fusarium sporotrichioides"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
 cDNA library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
 ; 3' end of cDNA cloned into XhoI site of pBluescript"
 44 a 61 c 53 g 56 t 1 others

BASE COUNT

44 a 61 c 53 g 56 t 1 others

ORIGIN

Query Match 6.8%; Score 75; DB 13; Length 215;
 Best Local Similarity 60.6%; Pred. No. 3e-11;
 Matches 123; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 496 TATTGGGATTGCTGTAGAGCCCTCTGTAGTGGCCCGGTAAAGGCATGTCACTTCCT 555
 1 TACTGGGAGTGGCGAAGCCTTCTGCTTGGAGCGGCAAGCTTAAAGTCAAGGCCCT 60
 Db 556 GTCAAGTCTGTAAACAAAGATGTGCTGACCTGCTTGTAGTGAACAGCAATGTCCAAAGTGC 615
 QY 61 GCTCTACTTGTGACAAAGATTAACCTATCACTAATCGAAGCGGTCAAGCGTTGT 120
 Db 616 TGTACGGTGTGACAGTGTACATGTGTACGACAAACAGCTTGGGCTGTAAAGATAT 675
 QY 121 GAGGATGTGTCTCTGCTTATGCTTACCACTACCTCCCGTGGCTGTCAAGACGAC 180
 Db 676 CTGCTATGCTTTCGCTGCTGC 698
 QY 181 CTGCTTACGCTTTCGCTGCTAC 203

RESULT 6 289 bp mRNA linear EST 10-JUL-2001
 B1191461
 LOCUS K3910fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 DEFINITION library Fusarium sporotrichioides cDNA clone K3910fs 5', mRNA
 sequence.

ACCESSION B1191461
 VERSION B1191461.1 GI:14665140
 KEYWORDS EST
 SOURCE Fusarium sporotrichioides.
 ORGANISM Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand
 M. and Roe, B.
 Analysis of a Fusarium sporotrichioides EST database

TITLE Unpublished (2001)
 JOURNAL Contact: Bruce A. Roe, University of Oklahoma, broeou.edu
 COMMENT Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762

FEATURES

source

Email: broeou.edu
 Contact Dr. Marian Beremand regarding clone availability. Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 323 6e-30 g1|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
 KPRECURSOR (EN
 KPRECURSOR (EN
 Seq primer: T3
 High quality sequence stop: 265.
 Location/Qualifiers

BASE COUNT

62 a 81 c 56 g 90 t

ORIGIN

Query Match 5.3%; Score 58.2; DB 13; Length 289;
 Best Local Similarity 61.6%; Pred. No. 3.8e-06;
 Matches 93; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 464 GTGGTCTCTGTGTACAGGTGTCACTCTGTTATTTGGATTGCTGTAGGCTCTCTGTA 523
 133 GTGCTCTCTGTGTGTACAGGTGTCACTCTGTTATTTGGATTGCTGTAGGCTCTCTGTA 192
 Db 524 GCTGGCCCGGTAAAGCCATGTGATGTTCTCTCTGTCAATGCTGTAAAGATGTGTA 583
 QY 193 CTGGAGCGGCAAGCTTAAAGTCAAGCGCCCTCTGCTGTGTGACAAAGATTAAC 252
 QY 584 CTGCCCTTATGTACAGCAATGTCCAAAGTGG 614
 Db 253 CTATCACTTACCTGAAAGCTGTCAAGCTTG 283

RESULT 7 299 bp mRNA linear EST 10-JUL-2001
 B1187393
 LOCUS a3b03fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 DEFINITION library Fusarium sporotrichioides cDNA clone a3b03fs 5', mRNA
 sequence.

ACCESSION B1187393
 VERSION B1187393.1 GI:14661072
 KEYWORDS EST
 SOURCE Fusarium sporotrichioides.
 ORGANISM Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand
 M. and Roe, B.
 Analysis of a Fusarium sporotrichioides EST database

TITLE Unpublished (2001)
 JOURNAL Other-ESTs: a3b03fs.f1
 COMMENT Contact: Bruce A. Roe, University of Oklahoma, broeou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762

REFERENCE Email: broeou.edu
 Contact Dr. Marian Beremand regarding clone availability. Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 329 1e-30 g1|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
 KPRECURSOR (EN
 KPRECURSOR (EN
 Seq primer: T3
 High quality sequence stop: 289.
 Location/Qualifiers

FEATURES

source

1. .299
 /organism="Fusarium sporotrichioides"

REFERENCE 1 (bases 1 to 541)
 AUTHORS Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
 TITLE Unpublished (2001)
 JOURNAL Development of Barley Transcriptome Resources
 COMMENT Contact: Waugh R, Marshall DF
 Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: ees@scri.sari.ac.uk.

FEATURES
 source
 1..541
 /organism="Hordeum vulgare"
 /cultivar="Optic"
 /db_xref="taxon:4513"
 /clone="EBR08.S0009.N14"
 /clone_lib="root, 3 week, drought-stressed, cv Optic, EBR08"
 /tissue_type="root"
 /dev_stage="3 week"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from roots of 3 week old drought stressed barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."

BASE COUNT 108 a 178 c 108 g 147 t

ORIGIN

Query Match 4.3%; Score 46.8; DB 14; Length 541;
 Best Local Similarity 60.0%; Pred. No. 0.015;
 Matches 78; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 53 CTGAATGGCTCTGCTAAATGATAGCAAGCTATGTCATGCTGCTGTAAGACT 112
 Db 235 CTGGCAGCCCTCTTCCGAAACGTTGCTTAAGCACTACCAAGTGGCTGCACTCACT 294

Qy 113 GGAATGGCTTACTGTGCAATCTGATCCACCTGTAAGTAAGCAAGATTACT 172
 Db 295 GGACTGGCCCACTCTCGCAAGACTGCTACCACTGCTTAAGCAGAACCTTACT 354

Qy 173 CTCAATGCTT 182
 Db 355 ACCAGTGTGT 364

RESULT 13
 AM285303 243 bp mRNA linear EST 19-JUL-2000
 LOCUS Lgi_237.F05.g1_A002 Light Grown 1 (LGI) sorghum bicolor cDNA, mRNA
 DEFINITION
 ACCESSION AM285303
 VERSION AM285303.1 GI:6675147
 KEYWORDS EST.
 SOURCE sorghum.
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 243)
 Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.
 An EST database from Sorghum: light-grown seedlings
 Unpublished (2000)
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210

Email: mmp@pratt@uga.edu
 Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
 Seq primer: T7
 High quality sequence start: 3
 High quality sequence stop: 243
 POLYA=Yes.

FEATURES
 source
 1..243
 /organism="Sorghum bicolor"
 /db_xref="taxon:4558"
 /clone_lib="Light Grown 1 (LGI)"
 /note="Organ: 10- to 14-day-old light-grown (greenhouse) seedlings; Vector: lambda Zap. Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."

BASE COUNT 51 a 66 c 53 g 73 t

ORIGIN

Query Match 4.1%; Score 45.6; DB 10; Length 243;
 Best Local Similarity 68.5%; Pred. No. 0.019;
 Matches 63; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 88 TATGTCATGCTGGTGAAGCACTGGAATGCCCTTCTGTCGAATGATCCACC 147
 Db 8 TACGACAGTCCGCTGATGCTGATGCTGACCTGCGCCGACCACTCGCTGGCTTACC 67

Qy 148 TGTAAAGTAAAGCAAGATTACTCTCAATG 179
 Db 68 TCGAAGTTTCCAACTTACTCTCCAGTG 99

RESULT 14
 AU013529 539 bp mRNA linear EST 03-AUG-1998
 LOCUS AU013529 Schizosaccharomyces pombe late log phase cDNA
 DEFINITION Schizosaccharomyces pombe cDNA clone spc08285, mRNA sequence.
 ACCESSION AU013529
 VERSION AU013529.1 GI:3368320
 KEYWORDS EST.
 SOURCE fission yeast.
 ORGANISM Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes.
 1 (bases 1 to 539)
 Moriwo, M. and Mita, K.
 Identification of expressed sequence tags of Schizosaccharomyces pombe
 Unpublished (1998)
 Contact: Mitsuoki Moriwo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: moriwo@nirs.go.jp.

FEATURES
 source
 1..539
 /organism="Schizosaccharomyces pombe"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc08285"
 /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /sex="h minus"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 130 a 119 c 101 g 185 t 4 others

ORIGIN

Matches	63	CONSERVATIVE	5	1970-1971

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Oy      86  TGTATGTCATGTGCTGTGAAGCACTGGAAATGGCCCTACTGTTGGGAATCTGGATCCA 145
Db      189  TTTGGGGGCAATGCGGAGGTCAAGAGTGAACCGGCCACACTAGTTGGCTTGATCTG 248

Oy      146  CCTGTAAAGTAAAGCAACGATCTACTCTGCATGTCCTTGC 185
           |||  |||  |||  |||  |||  |||  |||  |||
Db      249  CTGTGTCCTACTCTCAACCCCTACTACGCTCAATGATTC 288
           |||  |||  |||  |||  |||  |||  |||  |||

Search completed: June 17, 2003, 18:49:25
Job time : 1488.97 secs

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Search completed: June 17, 2003, 18:49:25
Job time : 1488.97 secs